

**Table S1: Typhoidal *Salmonella***

Serovar	CIP <sup>r</sup>	GyrA	GyrB	ParC	ParE	PMQR	Efflux	MIC (mg/L)	Reference
S. Typhi	S	Asp82Asn	-	-	-	-	ND	0.03	[76]
	I	-	-	Thr57Ser	-	-	ND	0.125	[76]
	R	Ser83Phe	-	Thr57Ser	-	-	No	1	[87]
	R	Ser83Tyr	-	Thr57Ser	-	-	No	2	[87]
	I-R	Ser83Tyr	-	Gly72Ser	-	-	No	0.25-0.38	[78]
	I – R	Ser83Phe	-	-	-	-	No/ND	0.19-6	[23, 34, 72, 74, 75, 76, 78, 85, 87, 100]
	R	Ser83Phe	-	-	-	<i>qnrB2</i>	ND	1	[79]
	R	Ser83Phe	-	-	-	<i>qnrS1</i>	ND	1-2	[102]
	R	Ser83Phe	-	Glu84Lys	ND	<i>qnrB</i>	No	>32	[78]
		Ser83Phe		Glu84Lys	ND	-	No	0.38->32	[78]
	I	Ser83Leu	-	-	-	-	ND	0.38-0.5	[34]
	R	Ser83Leu Asp87Asn	-	Ser80Ile	-	-	Yes	4	[87]
	I	Ser83Tyr	-	-	-	-	No/ND	0.25-0.5	[34, 72, 74, 78, 85, 87, 95]
	R	Ser83Tyr	-	-	-	<i>qnrS1</i>	Yes	4	[82, 85]
	S – I	Asp87Asn	-	-	-	-	No/ND	0.06-0.5	[72, 74, 85, 95]
	S – I	Asp87Gly	-	-	-	-	ND	0.06-0.5	[72]
	R	Asp87Tyr	-	-	-	<i>qnrS1</i>	ND	3	[34]
	S	Ser83Phe	-	-	Asp420Asn	-	ND	0.06	[72]
	I	Ser83Tyr	-	-	Ser493Phe	-	ND	0.38	[76]
	R	Ser83Phe Asp87Val	-	Ser80Ile	-	-	ND	>32	[34, 86]
	I – R	Ser83Phe Asp87Asn	-	-	-	-	ND	0.25-4	[74, 96]
	R	Ser83Phe Asp87Asn	-	Ser80Ile	-	-	No/ND	0.5- 63	[72, 74, 76, 78, 80, 87]
	R	Ser83Phe	-	Ser80Ile	-	-	No	2	[87]
	S	Glu133Gly	-	-	-	-	ND	0.06	[89, 90, 95]
	S	Glu133Gly	Ser426Gly	-	-	-	ND	NG	[95]
	R	Ser83Phe Asp87Asn	-	Thr57Ser Glu84Lys	-	-	ND	NG	[95]
	S	Ser83Phe Glu133Gly	-	Asp79Gly	-	-	ND	NG	[95]
	S	Ser83Phe Glu133Gly	-	-	Glu543Lys	-	ND	NG	[95]

	S	Ser83Phe Glu133Gly	-	-	Val560Gly	-	ND	NG	[95]	
	I	Ser83Phe Glu133Gly	-	-	Ile444Ser	-	ND	NG	[95]	
	S	Ser83Phe Glu133Gly	-	-	Tyr434Ser	-	ND	NG	[95]	
	R	Ser83Phe Asp87Gly	-	Glu92Lys	-	-	Yes	8-16	[85]	
	I	Ser83Phe Glu133Gly	-	-	-	-	ND	0.25-0.38	[32, 90]	
	R	Ser83Tyr Glu133Gly	-	-	-	<i>qnrS1</i>	ND	2	[34]	
	I	Ser83Phe Glu133Gly	Ala574Val	-	-	-	ND	0.38	[34]	
	I	Glu133GlySer83Phe	-	-	-	-	ND	0.5	[99]	
	I	†Gly133Glu Ser83Phe	-	-	-	-	ND	≤1	[91]	
	I – R	Ser83Phe	-	Trp106Gly	-	-	ND	ND	0.125-1	[96]
	R	Ser83Phe Asp87Asn Glu133Gly	-	Ser80Ile	-	-	ND	ND	7mm	[34]
	R	Ser83Phe Asp87Asn	Gly435Glu	Ser80Ile	-	-	ND	12	[76]	
	I	Ser83Phe	Gly435Ala	-	-	-	ND	0.15	[76]	
	I	Asp87Asn	Gly435Glu	-	-	-	ND	0.19	[76]	
	I	Ser83Phe	Gly435Glu	-	-	-	ND	0.25	[76]	
	I	Ser83Phe	Gly435Val	-	-	-	ND	0.5	[76]	
	I	-	Ser464Tyr	-	-	-	ND	0.125	[72, 93]	
	I	-	Ser464Phe	-	-	-	ND	0.125	[72, 93]	
	S	-	Ser464Thr	-	-	-	ND	0.06	[93]	
	I	Glu133Gly	Ser464Phe	-	-	-	ND	0.25	[99]	
S	-	Gln465Leu	-	-	-	ND	0.04-0.08	[72]		
S	-	Glu466Asp	-	-	-	ND	0.04	[72]		
S	-	Ala468Glu	-	-	-	ND	0.03	[72]		
S. Paratyphi A	I	Ser83Tyr	-	-	-	-	ND	21mm	[34, 71]	
	R	Ser83Phe Asp87Gly	ND	ND	-	-	ND	32	[100]	
	R	Ser83Phe Asp87Asn	-	Thr57Ser Glu84Lys	-	-	ND	NG	[95]	
		Ser83Phe			Ile444Ser				[95]	
	I – R	Ser83Phe	-		-	-	ND	0.125-1	[71, 95]	
	I	Ser83Phe	-	Thr57Ser	-	-	ND	0.5	[99]	
	I	Ser83Phe	-	Thr57Ser	-	-	ND	21-26 mm	[34, 95]	
	R – I	Asp87Asn	-	-	-	-	ND	0.125-1	[71]	
	I	Asp87Tyr	-	Thr57Ser	-	ND	ND	22 mm	[34]	
rat yp	I	Ser83Phe	-	-	-	-	ND	0.25-0.5	[34]	
		Ser83Phe	-	-	Ser498Thr		ND		[95]	

S. Paratyphi C	I	Ser83Tyr	-	-	-	-	ND	28mm / ≤1	[34] [91]
	I	Asp87Tyr	-	-	-	-	ND	21-28mm	[34]
	I	Asp87Asn	ND	ND	ND	ND	ND	≤ 1	[91]
	I	Asp87Gly	-	-	-	-	ND	22-26mm / ≤1	[34] [91]
	I	Arg47Ser Asp87Gly	ND	ND	ND	ND	ND	≤ 1	[91]
	I	Asp87Tyr	ND	ND	ND	ND	ND	≤ 1	[91]
	I	Asp87Gly	ND	ND	ND	ND	ND	≤ 1	[91]
	I	Asp87Asn	ND	ND	ND	ND	ND	≤ 1	[91]
	I	Ser83Phe Asp147Gly	ND	ND	ND	ND	ND	≤ 1	[91]

**Table S1: Mutations in the QRDRs of typhoidal *Salmonella*, namely *Salmonella* Typhi, *Salmonella* Paratyphi A, B and C.** Clinical and Laboratory Standards Institute (CLSI) guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of ≤ 0.06 mg/L. †Walther-Rausmussen and Hoiby [88] reported that *S. Typhi* has Gly instead of Glu at position 133 and the double mutant was Gly133Glu and Ser83Phe. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ND: not determined; NG: not given; S: susceptible; I: intermediate susceptibility; R: resistant.

Table S2: <i>Salmonella</i> Enteritidis								
CIP <sup>r</sup>	<i>gyrA</i>	<i>gyrB</i>	<i>parC</i>	<i>ParE</i>	PMQR	Efflux	MIC (mg/L)	References
I-R	Asp87Tyr	-	-	-	-	ND	0.09-1	[28, 34, 89, 106, 107, 108, 109, 110, 111, 113, 114, 115]
I-R	Asp87Gly	-	-	-	-	ND	0.125-1	[34, 89, 107, 108, 111, 112, 114, 115, 116]
I	Asp87Tyr	-	-	-	<i>qnrB</i>	ND	0.086	[113]
R	Asp87Tyr	-	-	-	<i>qnrS2</i>	ND	2	[28]
R	Asp87Tyr	-	-	-	<i>qnrS1</i>	ND	1	[108]
I	Asp87Asn	-	-	-	-	ND	0.032-0.25	[89, 91, 107, 110, 113, 115, 116, 117]
R	Asp87Asn	-	-	-	<i>qnrS1</i>	ND	1	[108, 112]
R	Asp87Asn	-	-	-	<i>aac(6')-lb-cr</i>	ND	2	[32]
I	Ser83Ile	-	-	-	-	ND	0.09-0.38	[108, 115]
I-R	Ser83Phe	-	-	-	-	ND	0.125-1	[28, 34, 106, 107, 108, 112, 113, 115, 116]
I	Ser83Phe	-	-	-	<i>qnrB</i>	ND	0.25	[32]
I	-	-	-	Val521Phe	<i>qnrS1</i>	ND	0.09	[108]
I	Ser83Phe	-	Thr57Ser	-	-	ND	0.25	[32]
I	Ser83Tyr	-	-	-	-	ND	0.25-0.5	[28, 34, 107, 108, 112, 115]
R	Ser83Tyr	-	-	-	<i>qnrS1</i>	ND	1-3	[34, 108, 115]
I	Ser83Tyr Asp87Gly	-	-	-	-	ND	0.125	[112]
I	Ser83Tyr Asp87Asn	-	-	-	-	ND	0.125-0.25	[34, 112]
S-I	Ser83Phe Asp87Asn	-	-	-	-	ND	0.064-0.125	[34, 112]
I	Ser83Phe Asp87Gly	-	-	-	-	ND	0.125	[112]
I	Ser83Phe Asp87Tyr	-	-	-	-	ND	4	[112, 115, 119]
R	Ser83Phe Asp87Ser	-	Ser67Cys Arg76Cys Cys80Arg	ND	-	Yes	256	[39]
I	Asp87Tyr Ala131Gly	-	-	-	-	ND	0.125	[112]
S	Ser97Pro	-	-	-	-	ND	0.06	[113]

**Table S2: Mutations in the QRDRs of *Salmonella* Enteritidis.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. Asp87Tyr substitution is predominant among *S. Enteritidis* isolates worldwide. PMQR determinants are rare, but present in isolates from Asia, Europe and America. The contribution of efflux to resistance has not been studied extensively. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ND: not determined; S: susceptible; I: intermediate susceptibility; R: resistant.

<b>Table S3: <i>Salmonella</i> Typhimurium</b>								
<b>CIP<sup>r</sup></b>	<b><i>gyrA</i></b>	<b><i>gyrB</i></b>	<b><i>parC</i></b>	<b><i>parE</i></b>	<b>PMQR</b>	<b>Efflux</b>	<b>MIC (mg/L)</b>	<b>References</b>
S-I	-	Glu466Asp	-	-	-	ND	0.06-0.25	[89, 126]
I	Asp87Asn	-	-	-	-	ND	0.125-0.25	[28, 34, 107, 112]
I	-	-	Thr57Ser	ND	-	ND	0.19	[34]
R	Asp87Asn	-	-	-	<i>aac(6')-Ib-cr</i>	ND	2-4	[124]
R	Asp87Asn	-	-	-	<i>aac(6')-Ib-cr, oqxA/B</i>	Yes	2-4	[153]
R	Asp87Asn	-	-	-	<i>aac(6')-Ib-cr, oqxA/B-qnrS1</i>	Yes	2- >32	[153]
R	Asp87Asn	-	-	-	<i>aac(6')-Ib-cr, qnrB</i>	Yes	2	[153]
I	Asp87Asn	-	Thr57Ser	-	<i>oqxA/B</i>	-	0.38	[32]
R	Asp87Asn	-	-	-	<i>oqxA/B</i>	Yes	4	[125, 153]
R	Asp87Gly	-	-	-	-	ND	1.12*	[108]
R	Asp87Gly	ND	-	ND	<i>aac(6')-Ib-cr</i>	ND	1	[134]
R	Asp87Tyr	-	-	-	<i>oqxAB</i>	ND	4	[125]
	Asp87Tyr	ND	-	ND	<i>qnrS1</i>	ND	0.25	[117]
I-R	Asp87Tyr	-	-	ND	-	ND	0.125-4	[34, 107, 117, 124]
R	Asp87Tyr	-	-	-	<i>aac(6')-Ib-cr</i>	ND	2-4	[124]
R	Asp87Tyr	-	-	-	<i>aac(6')-Ib-cr, qnrB</i>	ND	4	[124]
I	Ser83Tyr	-	Ser80Arg	-	-	ND	0.75	[32]
I	Ser83Tyr	-	-	-	-	No	0.12-1	[34, 89, 107, 112]
R	Ser83Tyr	ND	-	ND	<i>aac(6')-Ib-cr, qnrS1</i>	ND	8	[131]
I	Ser83Tyr	-	-	-	<i>oqxA/B</i>	ND	0.19	[32]
I	Ser83Phe	-	-	-	ND	ND	0.125-0.25	[107, 117]
R	Ser83Phe	-	-	-	<i>qnrS1</i>	ND	1.12*	[108]
R	Ser83Phe	-	-	-	<i>oqxA/B</i>	Yes	4	[125, 153]
I	-	-	-	Met438Ile	<i>qnrS1</i>	ND	0.38	[108]
I-R	Ser83Phe Asp87Asn	-	The57Ser Ser80Ile	ND	-	ND	0.19- >32	[34]
R	Ser83Phe Asp87Asn	-	The57Ser Ser80Arg	-	<i>aac(6')-Ib-cr</i>	ND	4	[124]
I	Ser83Phe Glu133Gly	-	-	ND	-	ND	0.125	[34]
R	Ser83Phe Asp87Asn	-	Ser80Arg	ND	-	ND	4-12	[34, 124, 125]
R	Ser83Phe Asp87Asn	-	Ser80Arg	-	<i>aac(6')-Ib-cr</i>	ND	4- >8	[124, 125]
R	Ser83Phe Asp87Asn		Ser80Arg	-	<i>qepA</i>	ND	>8	[125]
R	Ser83Phe Asp87Asn		Ser80Arg		<i>aac(6')-Ib-cr, oqxAB</i>		>8	[125]
R	Ser83Phe Asp87Gly	-	Ser80Arg	-	-	ND	4	[124]
R	Ser83Phe Asp87Gly Ala119Ser	ND	-	ND	-	Yes	512	[39]

**Table S3: Mutations in the QRDRs of *Salmonella* Typhimurium.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have

an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. While, *S. Typhimurium* isolates have been reported that do not have QRDR mutations but carry PMQR elements, only isolates that have QRDR mutations are discussed in this review. \*MIC is given as the geometrical mean value [108]. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ND: not determined; S: susceptible; I: intermediate susceptibility; R: resistant.

<b>Table S4: <i>Salmonella</i> Hadar</b>							
<b>CIP<sup>r</sup></b>	<b><i>gyrA</i></b>	<b><i>parC</i></b>	<b><i>parE</i></b>	<b>PMQR</b>	<b>Efflux</b>	<b>MIC (mg/L)</b>	<b>References</b>
S-I	Asp87Tyr	-	-	-	ND	0.047-0.125	[108, 133]
I	Asp87Tyr	Thr57Ser	-	-	ND	0.25	[28, 134]
I	Asp87Asn	-	-	-	ND	0.094-0.125	[34, 133]
I	Asp87Asn	-	ND	-	Yes	0.75	[106]
I	Asp87Asn	Thr57Ser	-	-	ND	0.125-0.25	[28, 107]
I	Asp87Asn	Thr57Ser Ser80Ile	ND	-	ND	0.19	[34]
I	Asp87Asn	Thr57Ser	ND	<i>qnrD1</i>	ND	29mm (ZOI)	[34]
I	Ser83Phe	Thr57Ser	ND	-	ND	0.25	[34]
R	Ser83Phe Asp87Asn	Ser80Ile	-	-	ND	8	[133]
I	Ser83Phe Asp87Asn	Thr57Ser	ND	-	ND	0.38	[34]
I	Ser83Tyr	-	-	<i>qnrD2</i>	ND	0.75	[133]
S	Ser83Tyr	-	-	-	ND	0.064-0.125	[133]
R	Asp87Tyr	Arg96Ser Pro98Lys		-	ND	1.12*	[108]

**Table S4: Mutations in the QRDR of *Salmonella* Hadar.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with an intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. None of the listed isolates carried a mutation in the *gyrB* gene. Similarly, no mutations were reported for the *parE* gene, but this was not studied in all isolates (as indicated by ND). \*MIC is given as the geometrical mean value [108]. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ZOI: zone of inhibition; ND: not determined; S: susceptible; I: intermediate susceptibility; R: resistant.

CIP <sup>r</sup>	<i>gyrA</i>	<i>parC</i>	<i>parE</i>	PMQR	Efflux	MIC (mg/L)	References
I	Ser83Tyr	-	-	-	ND	0.125	[133]
‡I	Ser83Phe	-			No	0.125-0.5	[41]
I-R	Ser83Phe	Ser80Ile	-	-	ND	0.19-8	[133]
R	Ser83Phe	Ser80Ile	-	-	ND	6 - >32	[133]
I	Asp87Asn	Thr57Ser	ND	-	ND	0.19	[34]
	Asp87Gly	-	ND	-	ND	0.047	[117]
R	Ser83Phe	Thr57Ser Ser80Ile	ND	-	ND	8-32	[34]
R	Ser83Phe Asp87Gly	Ser80Ile	-	-	No	6-8	[133]
‡R	Ser83Phe Asp87Tyr	Ser80Ile	-	-	Yes	4-8	[41, 133]
‡R	Ser83Phe Asp87Gly	Ser80Ile	-	-	Yes	3-8	[41, 133]
R	Ser83Phe Asp87Gly	Thr57Ser Ser80Ile	-	-	ND	9 -14 mm (ZOI)	[30, 34]
R	Ser83Phe Asp87Tyr	Thr57Ser Ser80Ile	-	-	ND	6 - ≥ 8	[34, 148]
R	Ser83Phe Asp87Asn	Thr57Ser Ser80Ile	ND	-	ND	8 - >32	[34]
‡R	Ser83Phe Asp87Asn	Ser80Ile	-	<i>aac(6')-Ib-cr</i>	ND	≥ 4	[144]
‡R	Ser83Phe Asp87Asn	Ser80Ile			Yes	8-16	[41]
R	Ser83Phe Asp87Tyr	Thr57Ser Ser80Ile	ND	<i>qnrB1</i>	ND	32	[34]
R	Ser83Phe Asp87Asn	Thr57Ser Ser80Ile	ND	<i>qnrD</i>	ND	24	[34]
S	-	Thr57Ser	ND	<i>qnrD</i>	ND	0.064	[34]
R	-	Thr57Ser	-	<i>qnrS1</i>	ND	8	[145]
I	-	Thr57Ser	ND	<i>qnrB1/qnrD</i>	ND	0.25	[34]

**Table S5: Mutations in the QRDRs of *Salmonella* Kentucky.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of ≤ 0.06 mg/L. None of the listed isolates was found to have a mutation in the *gyrB* gene. Similarly, no mutations were reported for the *parE* gene, but this was not studied in all isolates (as indicated by ND). CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ZOI: zone of inhibition; ND: not determined; S: susceptible; I: intermediate susceptibility; [R]: resistant. ‡*Salmonella* Kentucky isolates were confirmed to be ST198 [41, 144].

Table S6: <i>Salmonella</i> Indiana						
CIP <sup>r</sup>	GyrA	GyrB	ParC	PMQR	MIC (mg/L)	References
S-R	-	-	Thr57Ser	-	0.06-1	[107]
R	Ser83Leu	-	Ser80Ile	<i>aac(6')-Ib-cr</i>	4	[150]
R	Ser83Leu Asp87Asn	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr, oqxA</i>	32	[149]
R	Ser83Ile Asp87Asn	-	-	<i>aac(6')-Ib-cr</i>	2	[150]
I	Ser83Tyr	-	-	<i>qnrA</i>	0.25	[149]
R	Ser83Tyr	-	Ser80Ile	<i>aac(6')-Ib-cr</i>	2	[150]
R	Ser83Phe Asp87Gly	-	Thr57Ser	<i>oqxA</i>	128	[149]
R	Ser83Phe Asp87Gly	-	Thr57Ser Ser80Arg	<i>oqxAB</i>	8-64	[151]
R	Ser83Phe Asp87Asn	-	Thr57Ser Ser80Arg	<i>oqxAB</i>	32	[151]
R	Ser83Phe	-	Thr57Ser Ser80Arg	<i>oqxAB/ qepA</i>	32	[151]
R	Ser83Phe Asp87Asn	-	-	<i>aac(6')-Ib-cr/ oqxAB</i>	*>32	[153]
R	Ser83Phe Asp87Asn	-	Ser80Arg	<i>aac(6')-Ib-cr, oqxAB, qnrB</i>	*>32	[153]
R	Ser83Phe Asp87Asn	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr</i>	32-64	[151, 152]
R	Ser83Phe Asp87Asn	-	Thr57Ser Ser80Arg	-	8-16	[151]
R	Ser83Phe Asp87Asn	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr, oqxAB</i>	64-128	[151, 152]
R	Ser83Phe Asp87Asn	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr, oqxA, qnrA</i>	64	[149]
R	Ser83Phe Asp87Gly	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr oqxA, qnrA</i>	64	[149]
R	Ser83Phe Asp87Gly	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr, oqxAB</i>	64-128	[151, 152]
R	Ser83Phe Asp87Gly	-	Thr57Ser Ser80Arg	<i>aac(6')-Ib-cr</i>	16	[149]
R	Ser83Phe Asp87Gly	-	Thr57Ser Ser80Arg	-	8-128	[151, 152]
R	Ser83Phe Asp87Asn	-	Cys72Gly Ser80Arg	<i>aac(6')-Ib-cr, oqxAB</i>	*>32	[153]

**Table S6: Mutations in the QRDRs of *Salmonella* Indiana.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. None of the listed isolates was found to have a mutation in the *gyrB* and *parE* genes. \*Efflux inhibition resulted in a reduction of the MIC to >8 mg/L [153]; efflux was not studied for the other isolates. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; S: susceptible; I: intermediate susceptibility, R: resistant.

<b>CIP<sup>r</sup></b>	<b><i>gyrA</i></b>	<b><i>gyrB</i></b>	<b><i>parC</i></b>	<b>PMQR</b>	<b>MIC (mg/L)</b>	<b>References</b>
I-R	Ser83Tyr	-	Thr57Ser	-	0.25-1	[28, 32, 34, 114]
I	-	-	Thr57Ser	<i>qnrA1</i>	0.75	[34]
I	Ser83Tyr	Leu470Met	Thr57Ser	-	0.5	[28]
R	Ser83Tyr	-	Ser80Arg	-	2	[155]
R	Ser83Tyr	-	-	-	1-2	[155]
S	Ser83Phe	-	-	-	0.064	[112]
I	Ser83Leu	-	-	-	< 1	[91]
I	Asp87Tyr	-	-	-	< 1	[91, 156]
I-R	Asp87Asn	-	-	-	0.25-1	[114, 156]
I	Asp87Gly	-	Thr57Ser	-	0.25	[34]
I	Leu41Pro Asp87Tyr	-	-	-	< 1	[91]

**Table S7: Mutations in the QRDRs of *Salmonella* Infantis.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. The isolates reported by Hamidian et al. [91] showed MIC to CIP  $\leq 1$  mg/L, and, according to the updated CLSI guidelines, were thus classified as having intermediate susceptibility. None of the listed isolates was found to have a mutation in the *parE* gene. Efflux was not studied for any of the listed isolates. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; S: susceptible; I: intermediate susceptibility; R: resistant.

<b>Table S8: <i>Salmonella</i> Derby</b>							
<b>CIP<sup>r</sup></b>	<b><i>gyrA</i></b>	<b><i>gyrB</i></b>	<b><i>parC</i></b>	<b>PMQR</b>	<b>Efflux</b>	<b>MIC (mg/L)</b>	<b>References</b>
R	Asp87Gly	ND	-	<i>aac(6')-Ib-cr</i>	ND	1	[134]
I	Asp87Tyr	-	Thr57Ser	-	ND	0.12	[34]
I	Asp87Asn	-	Thr57Ser	-	ND	28mm (ZOI)	[34]
I	Ser83Phe	-	Thr57Ser	-	ND	0.19	[34]
R	Ser83Ile		ND	<i>oqxAB</i>	Yes	4	[153]
R	Ser83Tyr	-	-	<i>aac(6')-Ib-cr, oqxAB, qnrS2</i>	No	4	[153]
R	Ser83Tyr	-	ND	<i>oqxAB, qnrS8, qnrB</i>	Yes	2	[153]
R	Ser83Tyr	-	ND	<i>oqxAB, qnrS1, qnrB</i>	Yes	>32	[153]
R	Ser83Tyr	-		<i>qnrS1</i>	Yes	2	[153]
R	Asn78His	-	-	<i>aac(6')-Ib-cr, oqxAB, qnrS2</i>	No	2	[153]
I	-	-	Thr57Ser	<i>qnrB5</i>	ND	0.38	[34]

**Table S8: Mutations in the QRDRs of *Salmonella* Derby.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. None of the isolates was found to have a mutation in the *parE* gene. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ZOI: zone of inhibition; ND: not determined; S: susceptible; I: intermediate susceptibility; R: resistant.

<b>Table S9: <i>Salmonella</i> Newport</b>						
<b>CIP<sup>r</sup></b>	<b><i>gyrA</i></b>	<b><i>gyrB</i></b>	<b><i>parC</i></b>	<b>PMQR</b>	<b>MIC (mg/L)</b>	<b>References</b>
I	Asp87Gly	-	Thr57Ser	-	0.125	[28, 34]
S-R			Thr57Ser	-	0.06-1	[107]
R	Asp87Asn	-	-	-	1.12*	[108, 112]
R	Asp87Asn	-	Arg96Ser Pro98Thr	<i>qnrS1</i>	1.12*	[108]
I	Ser83Phe	-	Thr57Ser	-	0.19-0.25	[28, 34]
I-R	Ser83Tyr	-	Thr57Ser	-	0.25 -2	[28]
R	Ser83Tyr	-	Thr57Ser	<i>qnrS1/qnrS3</i>	4	[28]
I	Asp87Tyr	ND	Thr57Ser	-	0.125	[134]
I	-	-	Thr57Ser	<i>qnrS1</i>	0.25	[34]
I	Ser83Phe Asp87Asn	-	Thr57Ser	-	0.25	[34]

**Table S9: Mutations in the QRDRs of *Salmonella* Newport.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with an intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. Partially resistant and completely resistant isolates of *S. Newport* show equal prevalence for mutations of residues 83 or 87 and no preference for substitution by a specific residue. However, the Thr57Ser mutation is prevalent in *parC*. None of the isolates was found to have a mutation in the *parE* gene. Efflux was not studied for any of the listed isolates. \*MIC is given as the geometrical mean value [108]. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; ND: not determined; S: susceptible; I: intermediate susceptibility; R: resistant; ND: not determined.

<b>CIP<sup>r</sup></b>	<b><i>gyrA</i></b>	<b><i>gyrB</i></b>	<b><i>parC</i></b>	<b>PMQR</b>	<b>MIC (mg/L)</b>	<b>References</b>
I	Asp87Tyr	-	-	-	0.094	[133]
I	Asp87Tyr	-	-	<i>qnrB2</i>	0.25	[133]
I	Asp87Tyr	-	-	<i>qnrS1</i>	0.5	[133]
I	Asp87Tyr	-	-	-	0.094-0.75	[28, 34, 134]
I	Ser83Phe	-	-	-	0.25 – 0.5	[28, 30, 34, 134]
R	Ser83Phe			<i>qnrS1</i>	2	[166]
I	Asp87Tyr	-	-	-	0.094-0.125	[133]
I	Ser83Leu Asp87Asn	-	-	-	0.125	[28]
R	Ser83Phe Asp87Tyr	-	-	-	4	[119]

**Table S10: Mutations in the QRDRs of *Salmonella* Virchow.** CLSI guidelines [58] were followed to ensure a uniform classification of isolates showing ciprofloxacin resistance. According to these guidelines, resistant isolates have an MIC of 1–2 mg/L, isolates with intermediate susceptibility have an MIC of 0.12–0.5 mg/L, and susceptible isolates have an MIC of  $\leq 0.06$  mg/L. None of the isolates was found to have a mutation in the *parE* gene. Efflux was not studied for any of the listed isolates. The most prevalent mutation, Ser83Phe, was identified in isolates from Europe [28, 34], Africa [30] and Asia [134, 166]. CIP<sup>r</sup>: ciprofloxacin resistance phenotype; S: susceptible; I: intermediate susceptibility; R: resistant.